

## SEQUENCE LISTING

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<110> Kimoto, Norihiro
        Yamamoto, Hiroaki
        Nakajima, Takanori
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<130> SHZ-021

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<150> JP 2003-163015

<151> 2003-06-06

<150> JP 2003-113402

<151> 2003-04-17

<160> 25

<170> PatentIn version 3.1

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<212> DNA

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cat atc ctg tca caa ttg tta aaa caa gat tat aag gtt att gga act 96  
His Ile Leu Ser Gln Leu Leu Lys Gln Asp Tyr Lys Val Ile Gly Thr  
20 25 30

gtg aga tcc cat gaa aaa gaa gca aaa ttg cta aga caa ttt caa cat 144  
Val Arg Ser His Glu Lys Glu Ala Lys Leu Leu Arg Gln Phe Gln His  
35 40 45

aac cct aat tta act tta gaa att gtt ccg gac att tct cat cca aat 192  
Asn Pro Asn Leu Thr Leu Glu Ile Val Pro Asp Ile Ser His Pro Asn

50	55	60	
gct ttc gat aag gtt ctg cag aaa cgt gga cgt gag att agg tat gtt Ala Phe Asp Lys Val Leu Gln Lys Arg Gly Arg Glu Ile Arg Tyr Val 65 70 75 80			240
cta cac acg gcc tct cct ttt cat tat gat act acc gaa tat gaa aaa Leu His Thr Ala Ser Pro Phe His Tyr Asp Thr Thr Glu Tyr Glu Lys 85 90 95			288
gac tta ttg att ccc gcg tta gaa ggt aca aaa aac atc cta aat tct Asp Leu Leu Ile Pro Ala Leu Glu Gly Thr Lys Asn Ile Leu Asn Ser 100 105 110			336
atc aag aaa tat gca gca gac act gta gag cgt gtt gtt gtg act tct Ile Lys Lys Tyr Ala Ala Asp Thr Val Glu Arg Val Val Val Thr Ser 115 120 125			384
tct tgt act gct att ata acc ctt gca aag atg gac gat ccc agt gtg Ser Cys Thr Ala Ile Ile Thr Leu Ala Lys Met Asp Asp Pro Ser Val 130 135 140			432
gtt ttt aca gaa gag agt tgg aac gaa gca acc tgg gaa agc tgt caa Val Phe Thr Glu Glu Ser Trp Asn Glu Ala Thr Trp Glu Ser Cys Gln 145 150 155 160			480
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gct gcc tgg gag ttc aca aaa gag aat gaa gat cac atc aaa ttc aaa Ala Ala Trp Glu Phe Thr Lys Glu Asn Glu Asp His Ile Lys Phe Lys 180 185 190			576
cta aca aca gtc aac cct tct ctt ctt ttt ggt cct caa ctt ttc gat Leu Thr Thr Val Asn Pro Ser Leu Leu Phe Gly Pro Gln Leu Phe Asp 195 200 205			624
gaa gat gtg cat ggc cat ttg aat act tct tgc gaa atg atc aat ggc Glu Asp Val His Gly His Leu Asn Thr Ser Cys Glu Met Ile Asn Gly 210 215 220			672
cta att cat acc cca gta aat gcc agt gtt cct gat ttt cat tcc att Leu Ile His Thr Pro Val Asn Ala Ser Val Pro Asp Phe His Ser Ile 225 230 235 240			720
ttt att gat gta agg gat gtg gcc cta gct cat ctg tat gct ttc cag Phe Ile Asp Val Arg Asp Val Ala Leu Ala His Leu Tyr Ala Phe Gln 245 250 255			768
aag gaa aat acc gcg ggt aaa aga tta gtg gta act aac ggt aaa ttt Lys Glu Asn Thr Ala Gly Lys Arg Leu Val Val Thr Asn Gly Lys Phe 260 265 270			816
gga aac caa gat atc ctg gat att ttg aac gaa gat ttt cca caa tta Gly Asn Gln Asp Ile Leu Asp Ile Leu Asn Glu Asp Phe Pro Gln Leu 275 280 285			864

aga ggt ctc att cct ttg ggt aag cct ggc aca ggt gat caa gtc att 912  
 Arg Gly Leu Ile Pro Leu Gly Lys Pro Gly Thr Gly Asp Gln Val Ile  
 290 295 300

gac cgc ggt tca act aca gat aat agt gca acg agg aaa ata ctt ggc 960  
 Asp Arg Gly Ser Thr Thr Asp Asn Ser Ala Thr Arg Lys Ile Leu Gly  
 305 310 315 320

ttt gag ttc aga agt tta cac gaa agt gtc cat gat act gct gcc caa 1008  
 Phe Glu Phe Arg Ser Leu His Glu Ser Val His Asp Thr Ala Ala Gln  
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His Ile Leu Ser Gln Leu Leu Lys Gln Asp Tyr Lys Val Ile Gly Thr  
 20 25 30

Val Arg Ser His Glu Lys Glu Ala Lys Leu Leu Arg Gln Phe Gln His  
 35 40 45

Asn Pro Asn Leu Thr Leu Glu Ile Val Pro Asp Ile Ser His Pro Asn  
 50 55 60

Ala Phe Asp Lys Val Leu Gln Lys Arg Gly Arg Glu Ile Arg Tyr Val  
 65 70 75 80

Leu His Thr Ala Ser Pro Phe His Tyr Asp Thr Thr Glu Tyr Glu Lys  
 85 90 95

Asp Leu Leu Ile Pro Ala Leu Glu Gly Thr Lys Asn Ile Leu Asn Ser  
 100 105 110

Ile Lys Lys Tyr Ala Ala Asp Thr Val Glu Arg Val Val Val Thr Ser  
 115 120 125

Ser Cys Thr Ala Ile Ile Thr Leu Ala Lys Met Asp Asp Pro Ser Val  
 130 135 140

Val Phe Thr Glu Glu Ser Trp Asn Glu Ala Thr Trp Glu Ser Cys Gln  
 145 150 155 160

Ile Asp Gly Ile Asn Ala Tyr Phe Ala Ser Lys Lys Phe Ala Glu Lys  
 165 170 175



Ala	Ala	Trp	Glu	Phe	Thr	Lys	Glu	Asn	Glu	Asp	His	Ile	Lys	Phe	Lys	180	185	190
Leu	Thr	Thr	Val	Asn	Pro	Ser	Leu	Leu	Phe	Gly	Pro	Gln	Leu	Phe	Asp	195	200	205
Glu	Asp	Val	His	Gly	His	Leu	Asn	Thr	Ser	Cys	Glu	Met	Ile	Asn	Gly	210	215	220
Leu	Ile	His	Thr	Pro	Val	Asn	Ala	Ser	Val	Pro	Asp	Phe	His	Ser	Ile	225	230	235
Phe	Ile	Asp	Val	Arg	Asp	Val	Ala	Leu	Ala	His	Leu	Tyr	Ala	Phe	Gln	245	250	255
Lys	Glu	Asn	Thr	Ala	Gly	Lys	Arg	Leu	Val	Val	Thr	Asn	Gly	Lys	Phe	260	265	270
Gly	Asn	Gln	Asp	Ile	Leu	Asp	Ile	Leu	Asn	Glu	Asp	Phe	Pro	Gln	Leu	275	280	285
Arg	Gly	Leu	Ile	Pro	Leu	Gly	Lys	Pro	Gly	Thr	Gly	Asp	Gln	Val	Ile	290	295	300
Asp	Arg	Gly	Ser	Thr	Thr	Asp	Asn	Ser	Ala	Thr	Arg	Lys	Ile	Leu	Gly	305	310	315
Phe	Glu	Phe	Arg	Ser	Leu	His	Glu	Ser	Val	His	Asp	Thr	Ala	Ala	Gln	325	330	335
Ile	Leu	Lys	Lys	Glu	Asn	Arg	Leu									340		